



199	QY	CACTGCTGTGTGAAGCAGCACGCCAGTCACGGCGGCGCTCTCTCTCTGCGCGGAGGAGATC	258
61	Db	HisLeuLeuValIyHisSerGlnSerArgArgProSerSerTrpArgGlnGluIyHisIle	80
259	QY	ACCGGAGACCAAGGAGGAGGCGCTCGAGCTGATCAACGGCTACATCCAGAAAGATCAAGTCG	318
81	Db	ThrArgSerIyGlnGluIaLeuGluLeuIleAsnGlyIyTrIleGlnIyHisIySer	100
319	QY	GCAGAGGAGACATTTGAGTCTCTGCGCTCACAGTTCAGCGACTCGAGCTCAGCCAAAGGCC	378
101	Db	GlyGlnIuAspPheGlnSerLeuIaSerGlnPheSerAspCysSerSerAlaIyHisIa	120
379	QY	AGGGGAGACCTGGGTGGCTTTCCAGCAGAGGTTCAGATCCAGAAAGCCATTTGAAGACGCTCG	438
121	Db	ArgGlyAspLeuGlyProPheSerArgGlyGlnMetGlnIyAspProPheGlnAspAlaSer	140
439	QY	TTTCGGCTGCGGACGGGGGAGATGAGCGGGCGCGGTTCACGGATTCGCGCATCCACATC	498
141	Db	PheAlaLeuArgThrGlyGlnMetSerGlyProValPheThrAspSerGlyIleHisIle	160
499	QY	ATCTCTCCGCACTGAG	513
161	Db	IleLeuArgThrGlu	165

### RESULT 3

T08426  
P1ml protein homolog dodo - fruit fly (*Drosophila melanogaster*)  
C:Species: *Drosophila melanogaster*  
C>Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 09-Jul-2004  
C:Accession: T08426  
R:Maloszka, R.; de Couet, H.G.; Miklos, G.L.  
Proc. Natl. Acad. Sci. U.S.A. 95, 3731-3736, 1998  
A:Title: Data transferability from model organisms to human beings: insights from the fu  
A:Reference number: Z16415; MUID:98188272; PMID:9520435  
A:Accession: T08426  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-166 <MAL>  
A:Cross-references: UNIPROT:P54353; EMBL:AF017777; NID:g3004652; PIDN:AAC28408.1; PID:g3  
A:Experimental source: strain Cantons  
C:Genetics:  
A:Gene: dod  
A:Cross-references: FlyBase:FBgn0024251  
A:Introns: 20/1; 131/1  
C:Superfamily: yeast ESS1 protein; WW repeat homology  
A:Domain: 5-43/Domain: WW repeat homology <WW>

Alignment Scores:  
Pred. No.: 3.44e-25  
Score: 456.50  
Length: 166  
Matches: 93

US-10-687-361-1 (1-1014) x T08426 (1-166)	US-10-687-361-1 (1-1014) x T08426 (1-166)
Conservative: 16	Conservative: 16
Mismatches: 52	Mismatches: 52
Indels: 3	Indels: 3
Gaps: 2	Gaps: 2
Percent Similarity: 66.46%	Percent Similarity: 66.46%
Best Local Similarity: 56.71%	Best Local Similarity: 56.71%
Query Match: 24.23%	Query Match: 24.23%
DB: 2	DB: 2
25 ATGGCGGACGAGGAGAGCTCCGCCCGCTGGCGAAGCGCACA	25 ATGGCGGACGAGGAGAGCTCCGCCCGCTGGCGAAGCGCACA

Db  
1 MetProASPAlaGluGlnLeuProASP

85	CGAGTGTACTACTTCAACACACATCACTAACGCCAGCCAGTCGAGAGCGGCCACGC-----	138
21	MetSerTyrTyrLeuAsnMetTyrThrIysGluSerGlnTrpAspGlnProThrGluPro	40
139	GGCACAACGACGAGTCGTGTGGCAAAAAACGGCGACGGGGAG---CCTGCCAGGGTCCGCTGCC	195
41	AlaIysAlaThrGlyGlyGlySerAlaGlyGlyAspAlaProAspGluValHisCys	60
196	TCCGCACTCTGTGTGAAGCACACGACGAGTCACGGCGGCGCTCGTCTCTGGCGGCAGGAGAAG	255
61	LeuHisLeuLeuValIysHisIysGlySerArgArgProSerSerTrpArgGluAlaSer	80